

Tatiana A Vishnivetskaya

List of Publications by Year in descending order

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80
papers

16,666
citations

126907

33
h-index

85541

71
g-index

83
all docs

83
docs citations

83
times ranked

23824
citing authors

#	ARTICLE	IF	CITATIONS
1	Biogeochemical Characteristics of Earth's Volcanic Permafrost: An Analog of Extraterrestrial Environments. <i>Astrobiology</i> , 2022, 22, 812-828.	3.0	2
2	Draft Genome Sequences of 10 <i>Pseudomonas</i> sp. Isolates from the Active Layer of Permafrost in Ny Ålesund, Svalbard, Norway. <i>Microbiology Resource Announcements</i> , 2022, , e0020122.	0.6	0
3	Microbiome assembly in thawing permafrost and its feedbacks to climate. <i>Global Change Biology</i> , 2022, 28, 5007-5026.	9.5	34
4	Are permafrost microorganisms as old as permafrost?. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	17
5	Genomic reconstruction of fossil and living microorganisms in ancient Siberian permafrost. <i>Microbiome</i> , 2021, 9, 110.	11.1	17
6	A living bdelloid rotifer from 24,000-year-old Arctic permafrost. <i>Current Biology</i> , 2021, 31, R712-R713.	3.9	33
7	Comparative Metagenomics of the Active Layer and Permafrost from Low-Carbon Soil in the Canadian High Arctic. <i>Environmental Science & Technology</i> , 2021, 55, 12683-12693.	10.0	10
8	Eight Metagenome-Assembled Genomes Provide Evidence for Microbial Adaptation in 20,000- to 1,000,000-Year-Old Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0097221.	3.1	13
9	Permafrost Active Layer Microbes From Ny Ålesund, Svalbard (79°N) Show Autotrophic and Heterotrophic Metabolisms With Diverse Carbon-Degrading Enzymes. <i>Frontiers in Microbiology</i> , 2021, 12, 757812.	3.5	7
10	Insights into community of photosynthetic microorganisms from permafrost. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	6
11	Free Iron and Iron-Reducing Microorganisms in Permafrost and Permafrost-Affected Soils of Northeastern Siberia. <i>Eurasian Soil Science</i> , 2020, 53, 1455-1468.	1.6	4
12	Thaumarchaea Genome Sequences from a High Arctic Active Layer. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
13	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. <i>Genetics</i> , 2020, 214, 719-733.	2.9	20
14	Predominance of Anaerobic, Spore-Forming Bacteria in Metabolically Active Microbial Communities from Ancient Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	25
15	Methane in Gas Shows from Boreholes in Epigenetic Permafrost of Siberian Arctic. <i>Geosciences (Switzerland)</i> , 2019, 9, 67.	2.2	23
16	Metagenome-Assembled Genome of USC ¹ AHI, a Potential High-Affinity Methanotroph from Axel Heiberg Island, Canadian High Arctic. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	8
17	Draft Genome Sequence of <i>Microbacterium</i> sp. Gd 4-13, Isolated from Gydanskiy Peninsula Permafrost Sediments of Marine Origin. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
18	Metagenomes from Late Pleistocene Ice Complex Sediments of the Siberian Arctic. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0

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19	Microbial community structure with trends in methylation gene diversity and abundance in mercury-contaminated rice paddy soils in Guizhou, China. <i>Environmental Sciences: Processes and Impacts</i> , 2018, 20, 673-685.	3.5	36
20	Earth's perennially frozen environments as a model of cryogenic planet ecosystems. <i>Permafrost and Periglacial Processes</i> , 2018, 29, 246-256.	3.4	14
21	Methanogens in the Antarctic Dry Valley permafrost. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	22
22	MICROBIAL DIVERSITY OF SIBERIAN PERMAFROST. , 2018, , .		0
23	Atmospheric CH_4 oxidation by Arctic permafrost and mineral cryosols as a function of water saturation and temperature. <i>Geobiology</i> , 2017, 15, 94-111.	2.4	14
24	Metagenomic analyses of the late Pleistocene permafrost – additional tools for reconstruction of environmental conditions. <i>Biogeosciences</i> , 2016, 13, 2207-2219.	3.3	59
25	Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
26	Surface reflectance degradation by microbial communities. <i>Journal of Building Physics</i> , 2016, 40, 263-277.	2.4	3
27	Effects of simulated spring thaw of permafrost from mineral cryosol on CO_2 emissions and atmospheric CH_4 uptake. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2015, 120, 1764-1784.	3.0	28
28	An active atmospheric methane sink in high Arctic mineral cryosols. <i>ISME Journal</i> , 2015, 9, 1880-1891.	9.8	92
29	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. <i>Microbial Ecology</i> , 2015, 69, 333-345.	2.8	20
30	Changes in northern Gulf of Mexico sediment bacterial and archaeal communities exposed to hypoxia. <i>Geobiology</i> , 2015, 13, 478-493.	2.4	16
31	Improved Yield of High Molecular Weight DNA Coincides with Increased Microbial Diversity Access from Iron Oxide Cemented Sub-Surface Clay Environments. <i>PLoS ONE</i> , 2014, 9, e102826.	2.5	25
32	Draft Genome Sequences of 10 Strains of the Genus <i>Exiguobacterium</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	31
33	High-Performance Bioanode Development for Fermentable Substrates via Controlled Electroactive Biofilm Growth. <i>ChemElectroChem</i> , 2014, 1, 1940-1947.	3.4	17
34	Diversity and genomic insights into the uncultured <i>Candidatus Chloroflexi</i> from the human microbiota. <i>Environmental Microbiology</i> , 2014, 16, 2635-2643.	3.8	55
35	Commercial DNA extraction kits impact observed microbial community composition in permafrost samples. <i>FEMS Microbiology Ecology</i> , 2014, 87, 217-230.	2.7	89
36	Metagenomes from Thawing Low-Soil-Organic-Carbon Mineral Cryosols and Permafrost of the Canadian High Arctic. <i>Genome Announcements</i> , 2014, 2, .	0.8	20

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37	Biogeography of the ecosystems of the healthy human body. <i>Genome Biology</i> , 2013, 14, R1.	9.6	540
38	Microbial Communities Involved in Biological Ammonium Removal from Coal Combustion Wastewaters. <i>Microbial Ecology</i> , 2013, 66, 49-59.	2.8	17
39	Environmental proteomics reveals early microbial community responses to biostimulation at a uranium- and nitrate-contaminated site. <i>Proteomics</i> , 2013, 13, 2921-2930.	2.2	71
40	Host genetic and environmental effects on mouse intestinal microbiota. <i>ISME Journal</i> , 2012, 6, 2033-2044.	9.8	206
41	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	27.8	9,614
42	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	27.8	2,249
43	Microbes in thawing permafrost: the unknown variable in the climate change equation. <i>ISME Journal</i> , 2012, 6, 709-712.	9.8	153
44	Anaerobic High-Throughput Cultivation Method for Isolation of Thermophiles Using Biomass-Derived Substrates. , 2012, 908, 153-168.		11
45	Characterization of the Deltaproteobacteria in contaminated and uncontaminated stream sediments and identification of potential mercury methylators. <i>Aquatic Microbial Ecology</i> , 2012, 66, 271-282.	1.8	26
46	Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Tennessee Streams. <i>Applied and Environmental Microbiology</i> , 2011, 77, 302-311.	3.1	137
47	Enhancement in current density and energy conversion efficiency of 3-dimensional MFC anodes using pre-enriched consortium and continuous supply of electron donors. <i>Bioresource Technology</i> , 2011, 102, 5098-5104.	9.6	40
48	Extended survival of several organisms and amino acids under simulated martian surface conditions. <i>Icarus</i> , 2011, 211, 1162-1178.	2.5	38
49	Complete Genome Sequence of the Thermophilic Bacterium <i>Exiguobacterium</i> sp. AT1b. <i>Journal of Bacteriology</i> , 2011, 193, 2880-2881.	2.2	47
50	Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. <i>Microbial Ecology</i> , 2010, 60, 784-795.	2.8	51
51	<i>Caldicellulosiruptor obsidiansis</i> sp. nov., an Anaerobic, Extremely Thermophilic, Cellulolytic Bacterium Isolated from Obsidian Pool, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1014-1020.	3.1	91
52	Microbial Community Changes in Response to Ethanol or Methanol Amendments for U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5728-5735.	3.1	38
53	Donor-Dependent Extent of Uranium Reduction for Bioremediation of Contaminated Sediment Microcosms. <i>Journal of Environmental Quality</i> , 2009, 38, 53-60.	2.0	26
54	The <i>Exiguobacterium</i> genus: biodiversity and biogeography. <i>Extremophiles</i> , 2009, 13, 541-555.	2.3	202

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55	Integrating engineering design improvements with exoelectrogen enrichment process to increase power output from microbial fuel cells. <i>Journal of Power Sources</i> , 2009, 191, 520-527.	7.8	86
56	Microbial Communities in Subpermafrost Saline Fracture Water at the Lupin Au Mine, Nunavut, Canada. <i>Microbial Ecology</i> , 2009, 58, 786-807.	2.8	52
57	Controlling accumulation of fermentation inhibitors in biorefinery recycle water using microbial fuel cells. <i>Biotechnology for Biofuels</i> , 2009, 2, 7.	6.2	72
58	Improving power production in acetate-fed microbial fuel cells via enrichment of exoelectrogenic organisms in flow-through systems. <i>Biochemical Engineering Journal</i> , 2009, 48, 71-80.	3.6	110
59	Proteomic Insights: Cryoadaptation of Permafrost Bacteria. <i>Soil Biology</i> , 2009, , 169-181.	0.8	4
60	Viable Cyanobacteria and Green Algae from the Permafrost Darkness. <i>Soil Biology</i> , 2009, , 73-84.	0.8	26
61	Effect of Growth Temperature and Culture Medium on the Cryotolerance of Permafrost <i>Exiguobacterium Sibiricum</i> 255-15 by Proteome-Wide Mass Mapping. <i>The Open Proteomics Journal</i> , 2009, 2, 8-19.	0.4	1
62	Bacteria in Permafrost. , 2008, , 83-102.		53
63	Elucidating Biogeochemical Reduction of Chromate via Carbon Amendments and Soil Sterilization. <i>Geomicrobiology Journal</i> , 2007, 24, 125-132.	2.0	7
64	Effect of low temperature and culture media on the growth and freeze-thawing tolerance of <i>Exiguobacterium</i> strains. <i>Cryobiology</i> , 2007, 54, 234-240.	0.7	51
65	Microbial Populations in Antarctic Permafrost: Biodiversity, State, Age, and Implication for Astrobiology. <i>Astrobiology</i> , 2007, 7, 275-311.	3.0	243
66	Bacterial Community in Ancient Siberian Permafrost as Characterized by Culture and Culture-Independent Methods. <i>Astrobiology</i> , 2006, 6, 400-414.	3.0	143
67	Characterization of <i>Exiguobacterium</i> isolates from the Siberian permafrost. Description of <i>Exiguobacterium sibiricum</i> sp. nov.. <i>Extremophiles</i> , 2006, 10, 285-294.	2.3	124
68	<i>Psychrobacter cryohalolentis</i> sp. nov. and <i>Psychrobacter arcticus</i> sp. nov., isolated from Siberian permafrost. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1285-1291.	1.7	169
69	Calmodulin kinase II inhibition protects against structural heart disease. <i>Nature Medicine</i> , 2005, 11, 409-417.	30.7	526
70	Putative Transposases Conserved in <i>Exiguobacterium</i> Isolates from Ancient Siberian Permafrost and from Contemporary Surface Habitats. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6954-6962.	3.1	43
71	Chapter 10. Viable Phototrophs: Cyanobacteria and Green Algae from the Permafrost Darkness. , 2005, , 140-158.		7
72	Microbial Life In Permafrost. , 2004, , 151-169.		7

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73	The resistance of viable permafrost algae to simulated environmental stresses: implications for astrobiology. <i>International Journal of Astrobiology</i> , 2003, 2, 171-177.	1.6	29
74	The Evolution of A β Peptide Burden in the APP23 Transgenic Mice: Implications for A β Deposition in Alzheimer Disease. <i>Molecular Medicine</i> , 2001, 7, 609-618.	4.4	99
75	Low-temperature recovery strategies for the isolation of bacteria from ancient permafrost sediments. <i>Extremophiles</i> , 2000, 4, 165-173.	2.3	163
76	The deep cold biosphere: facts and hypothesis. <i>FEMS Microbiology Reviews</i> , 1997, 20, 277-290.	8.6	201
77	The deep cold biosphere: facts and hypothesis. <i>FEMS Microbiology Reviews</i> , 1997, 20, 277-290.	8.6	19
78	Permafrost microbiology. <i>Permafrost and Periglacial Processes</i> , 1995, 6, 281-291.	3.4	84
79	Genomic and Expression Analyses of Cold-Adapted Microorganisms. , 0, , 126-155.		22
80	Microbial Carbon Cycling in Permafrost. , 0, , 181-199.		1